Alzheimer's & Dementia 14 (2018) 848-857

Featured Article

Disentangling the biological pathways involved in early features of Alzheimer's disease in the Rotterdam Study

Shahzad Ahmad[a], Christian Bannister[b], Sven J. van der Lee[a], Dina Vojinovic[a], Hieab H. H. Adams[a,c], Alfredo Ramirez[d,e,f], Valentina Escott-Price[b], Rebecca Sims[b], Emily Baker[b], Julie Williams[b], Peter Holmans[b], Meike W. Vernooij[a,c], M. Arfan Ikram[a,c], Najaf Amin[a], Cornelia M. van Duijn[a,*]

[a]*Department of Epidemiology, Erasmus Medical Centre, Rotterdam, The Netherlands*
[b]*MRC Centre for Neuropsychiatric Genetics & Genomics, Institute of Psychological Medicine and Clinical Neurosciences, Cardiff University, Cardiff, United Kingdom*
[c]*Department of Radiology and Nuclear Medicine, Erasmus Medical Centre, Rotterdam, The Netherlands*
[d]*Department for Neurodegenerative Diseases and Geriatric Psychiatry, University Hospital Bonn, Bonn, Germany*
[e]*Department of Psychiatry and Psychotherapy, University Hospital Cologne, Cologne, Germany*
[f]*Institute of Human Genetics, University of Bonn, Bonn, Germany*

Abstract

Introduction: Exploring the role of Alzheimer's disease (AD) implicated pathways in the predementia phase may provide new insight for preventive and clinical trials targeting disease specific pathways.

Methods: We constructed weighted Genetic risk scores, first based on 20 genome-wide significant AD risk variants and second clustering these variants within pathways. Risk scores were investigated for their association with AD, mild cognitive impairment, and brain magnetic resonance imaging phenotypes including white matter lesions, hippocampal volume, and brain volume.

Results: The risk score capturing *endocytosis* pathway was significantly associated with mild cognitive impairment ($P = 1.44 \times 10^{-4}$). *Immune response* ($P = .016$) and *clathrin/AP2 adaptor complex* pathway ($P = 3.55 \times 10^{-3}$) excluding apolipoprotein E also showed modest association with white matter lesions but did not sustain Bonferroni correction ($P = 9.09 \times 10^{-4}$).

Discussion: Our study suggests that the clinical spectrum of early AD pathology is explained by different biological pathways, in particular, the *endocytosis, clathrin/AP2 adaptor complex,* and *immune response* pathways, that are independent of apolipoprotein E (*APOE*).

Keywords: Genetic risk score; Alzheimer's disease; White matter lesions; Mild cognitive impairment; Endocytosis; Immune response

1. Introduction

Alzheimer's disease (AD) is a heterogeneous and genetically complex disease with high heritability (56–79%) [1]. It has been known since the end of the previous century that a polymorphism in the apolipoprotein E (*APOE*) gene is the strongest common genetic risk factor [2–4]. This finding fueled speculations on the role of the *lipid metabolism* and *cholesterol transport* pathway in AD in addition to the *amyloid cascade* and *tau phosphorylation* mechanism [5,6]. Furthermore, large-scale genome-wide association studies have discovered more than 20 novel common genetic variants that influence the risk of late-onset AD [7–13]. These

The authors have declared that no conflict of interest exists.

*Corresponding author. Tel.: +31107043394; Fax: +31107044657.
E-mail address: c.vanduijn@erasmusmc.nl

https://doi.org/10.1016/j.jalz.2018.01.005

common genetic variants have been mapped to eight biological pathways including *immune response, endocytosis, cholesterol transport, hematopoietic cell lineage, protein ubiquitination, hemostasis, clathrin/AP2 adaptor complex,* and *protein folding*, each having a distinct biological function [14–16]. These eight pathways are not independent in a way that genes may be part of more than one biological pathway. For instance, *APOE* is part of four of the eight pathways namely *cholesterol transport, hematopoietic cell lineage, clathrin/AP2 adaptor complex,* and *protein folding* pathways; clusterin (*CLU*) encoding for apolipoprotein J is involved in six pathways; phosphatidylinositol binding clathrin assembly protein (*PICALM*) and complement factor 1 (*CR1*) are involved in two pathways [14–16].

These diverse biological pathways may be responsible for the clinically heterogeneous manifestation of AD [17–19], which include endophenotypes such as changes in structural and functional magnetic resonance imaging (MRI) phenotypes, most notably hippocampal volume, total brain volume, and white matter lesions [20–23]. Furthermore, these biological pathways may also modulate the prodromal stages of AD such as mild cognitive impairment (MCI) [24–26]. Owing to heterogeneity during the predementia phase, one important unanswered question is whether the different biological pathways that are implicated in AD relate to the pleiotropy of clinical endophenotypes. We hypothesized that some biological pathways are involved in distinct clinical endophenotypes, whereas others may be involved in multiple or even all. Disentangling the connection of biological pathways to various aspects of AD-related early pathology may be a crucial step toward improving our understanding of the pathogenesis of AD during the predementia stage and a first step toward a more informative and powerful readout for preventive and therapeutic trials targeting specific pathways.

The present study aims to capture the different biological pathways involved in AD using genetic risk scores to evaluate their role in AD and predementia endophenotypes including MCI, white matter lesions, and total brain and hippocampal volume.

2. Methods

2.1. Study population

This study included samples from the Rotterdam Study (RS). The RS is a prospective population-based study [27] designed to investigate the etiology of age-related disorders. At the baseline examination in 1990 to 1993, study recruited 7983 subjects ≥55 years of age from the Ommoord district of Rotterdam (RS-I). At the baseline entry and after every 3 to 4 years, all the study participants were extensively interviewed and physically examined at the dedicated research center. During 2000 to 2001, the baseline cohort (RS-I) was expanded by adding 3011 subjects ≥55 years of age, who were not yet part of RS-I (RS-II). Second expansion of RS was performed by recruiting 3932 persons having ≥45 years of age during 2006 to 2008 (RS-III). The study has been approved by the Medical Ethical Committee of Erasmus Medical Center and by the Ministry of Health, Welfare and Sport of the Netherlands. Written informed consents were also obtained from each study participant to participate and to collect information from their treating physicians. Details of AD, dementia, and MCI diagnosis are provided in the Supplementary Information. In the present study for AD cross-sectional analysis, we included in total 1270 late-onset AD cases and 7623 controls (age at last follow-up ≥ 65 years and dementia free) whose follow-up information is complete until 2009 to 2013 in RS-I, RS-II, and RS-III cohorts. This AD sample includes 1057 incident and 213 prevalent AD cases. For prospective AD analysis, 10,370 dementia-free (normal) participants were also included in the study from all three RS cohorts at their baseline and were subsequently followed until 2009 to 2013, to analyze their progression into AD (average 11 years of follow-up). In the MCI data set, we included 360 MCI cases and 3245 cognitively normal controls from the first extensive cognitive assessment conducted between 2002 and 2005 in RS-I and RS-II cohorts. MRI was implemented in 2005 in RS cohorts, and 5899 persons came for MRI scanning until 2015. After excluding subjects with stroke and/or dementia (n = 251) at time of scanning, poor imaging quality (n = 313), and missing genotyping information (n = 814), we retained 4521 cognitively normal individuals in the MRI sample (Table 1).

2.2. Genotyping

Blood was drawn for genotyping from participants of RS cohorts during their first visit, and DNA genotyping was performed at the internal genotyping facility of the Erasmus Medical Center, Rotterdam. All samples were genotyped with the 550K, 550K duo, or 610K Illumina arrays. Genotyping quality control criteria include call rate <95%, Hardy-Weinberg equilibrium $P < 1.0 \times 10^{-6}$, and minor allele frequency <1%. Moreover, study samples with excess autosomal heterozygosity, call rate <97.5%, ethnic outliers, and duplicate or family relationships were excluded during quality control analysis. Genetic variants were imputed from the Haplotype Reference Consortium reference panel (version 1.0) [28], using the Michigan imputation server [29]. The server uses SHAPEIT2 (v2.r790) [30] to phase the genotype data and performs imputation with Minimac 3 software [31]. For this study, we used genetic variants that had imputation quality (R^2) > 0.5.

2.3. MRI scanning

2.3.1. Image acquisition

MRI scanning is assessed on a 1.5-T MRI unit with a dedicated eight-channel head coil (Signa HD platform; GE

Table 1
Cohort characteristics

Characteristics	RS-I	RS-II	RS-III	Total
AD data set (N)	5854	2062	977	8893
Late-onset AD	1118	134	18	1270
AD free controls	4736	1928	959	7623
Age-of-onset (SD), years	84.58 (6.8)	82.75 (6.7)	78.54 (9.5)	84.30 (6.8)
Age of controls (SD), years	82.87 (6.9)	76.52 (6.4)	69.15 (5.7)	79.53 (8.2)
Female (%)	3526 (60)	1133 (55)	569 (58)	5228 (59)
MCI data set (N)	2178	1427		3605
MCI cases	235	125	-	360
Controls	1943	1302	-	3245
Age (SD), years	74.79 (5.7)	67.53 (6.9)	-	71.9 (7.2)
Female (%)	1271(58.4)	786 (55.1)	-	2057 (57%)
MRI data set (N)	968	1068	2485	4521
Age (SD), years	78.89 (4.9)	69.34 (5.9)	57.21 (6.4)	64.72 (10.8)
Female (%)	556 (58)	565 (53)	1390 (56)	2511 (56)

Abbreviations: AD, Alzheimer's disease; MCI, mild cognitive impairment; MRI, magnetic resonance imaging; RS, Rotterdam Study (cohort I, II, and III); SD, standard deviation.

Healthcare, Milwaukee, WI) since the induction of a dedicated MRI machine in the RS. The MRI protocol was based on several high-resolution axial sequences, including a T1-weighted (slice thickness 0.8 mm), T2-weighted (1.6 mm), and fluid-attenuated inversion recovery sequence (2.5 mm). A detailed description of the MRI protocol is described previously [32].

2.3.2. Image processing

We excluded 251 persons with stroke and/or dementia from the total 5899 subjects because this may affect image processing. All T1 images were segmented into the supratentorial gray matter, white matter, and cerebrospinal fluid using a *k*-nearest neighbor algorithm [33]. White matter lesions were segmented based on T1 tissue maps and an automatically detected threshold for the intensity of fluid-attenuated inversion recovery scans [34]. The hippocampus was segmented using a fully automated method, as described previously [35]. Semiquantitative MRI postprocessing software was used to measure intracranial volume and brain volume, which included Elastix and custom-built software [36]. To calculate intracranial volume, non–brain tissues (skull, eyes, and dura) were removed by nonlinearly registering all brain scans to a manually created template in which non–brain tissues were masked [33,36,37]. In all MRI scans, after visual inspection of all segmentations, additional 313 subjects were excluded because of poor quality.

2.4. Statistical analysis

2.4.1. Genetic risk score computation

To construct the risk score, we selected late-onset AD-associated single-nucleotide polymorphisms (SNPs) reaching genome-wide significance level ($P < 5.0 \times 10^{-8}$; Supplementary Table 1), including one rare *TREM2* variant [7,38]. In common variants, we considered only variants identified by the International Genomics of Alzheimer's Project (IGAP) meta-analyses. In addition, we considered *APOE* ε4 (rs429358) variant for risk score construction. From a total of 21 SNPs, the *HLA-DRB1-HLA-DRB5* (rs9271192) variant was excluded from risk score calculation because of its low imputation quality ($R^2 = 0.31$) in the RS. This led to a final selection of 20 independent genome-wide significant AD-associated variants. Weighted genetic risk score was constructed using the effect sizes (log of odds ratio) of the genome-wide significant variants from the IGAP meta-analysis [7] as weights and their respective allele dosages from imputed genotype data of our study cohorts. Risk score was constructed as the sum of the products of SNP dosages and their corresponding weights in R software (https://www.R-project.org/). We constructed genetic risk score in two ways: (1) combining all 20 selected variants and (2) clustering the variants into their respective pathways.

2.4.1.1. Combined genetic risk score

Combined genetic risk score (GRS1) was constructed in two ways, that is, (1) using all the 20 selected SNPs and (2) excluding the *APOE* ε4 variant to identify the joint independent effect of all other genome-wide significant SNPs.

2.4.1.2. Pathway-specific genetic risk score

For pathway-specific genetic risk score (GRS2), the genome-wide significant AD SNPs were divided into pathways (*immune response, endocytosis, cholesterol transport, hematopoietic cell lineage, protein ubiquitination, hemostasis, clathrin/AP2 adaptor complex, and protein folding pathway*) identified by Jones et al. [16] (Supplementary Table 2). Classifying genome-wide significant AD SNPs into pathways, we also used information from Guerreiro et al. [14], in which the authors reviewed the possible division of known AD-associated genes into biological pathways [14]. Furthermore, the GeneNetwork database (http://genenetwork.nl/) was used to confirm the allocated pathways. Of the 20 SNPs, 14 could be clustered into seven nonmutually exclusive pathways

Table 2
Results of association of AD with risk scores

SNP cluster*	Including *APOE*			Excluding *APOE*		
	β	SE	*P* value	β	SE	*P* value
GRS1 (combined)	0.73	0.040	6.53×10^{-74}	0.69	0.101	1.12×10^{-11}
Immune response	-	-	-	0.69	0.166	3.20×10^{-5}
Endocytosis	-	-	-	0.75	0.171	1.28×10^{-5}
Cholesterol transport	0.71	0.042	3.22×10^{-64}	0.39	0.219	.077
Hematopoietic cell lineage†	0.73	0.042	5.16×10^{-66}	-	-	-
Hemostasis	-	-	-	0.50	0.292	.090
Clathrin/AP2 adaptor complex	0.72	0.042	4.68×10^{-65}	0.50	0.236	.036
Protein folding†	0.72	0.042	2.96×10^{-64}	-	-	-

Abbreviations: β, regression coefficient; APOE, apolipoprotein E; GRS1, combined genetic risk score; GRS2, pathway-specific genetic risk score; RS, Rotterdam Study; SE, standard error; SNP, single-nucleotide polymorphism.

NOTE. Multiple testing correction by Bonferroni [0.05/(5 phenotypes × 11 risk scores); $P < 9.09 \times 10^{-4}$] was considered significant.

*Logistic regression model adjusted for age and sex in the RS (N = 1270 cases).

†Only one SNP available in excluding *APOE* GRS2.

(Supplementary Table 2). Similar to GRS1, we also constructed GRS2 with and without the *APOE* ε4 variant. The *APOE* ε4 variant was grouped under four pathways including *cholesterol transport [14]*, *hematopoietic cell lineage*, *clathrin/AP2 adaptor complex,* and *protein folding [16]*. GRS2 was constructed for only those pathways which could be assigned at least two SNPs; therefore, *protein ubiquitination* pathway, which contained only one SNP, was excluded from all analyses, while *hematopoietic cell lineage and protein folding* pathways were also not considered in the analyses excluding the *APOE* ε4 variant.

2.4.2. Association analyses of GRS1 and GRS2

To test the association of AD and MCI with the risk scores, we used logistic regression analysis in R software (www.R-project.org), using disease status as the outcome, risk scores as predictor, and age and sex as covariates. To assess the possible inflation of association results between AD and risk scores, we repeated the association analysis excluding 625 AD cases who were part of the IGAP meta-analysis [7] from total 1270 AD cases of the RS cohort. Furthermore, we performed prospective analysis using the Cox-proportional hazards model (N = 1057 incident AD cases) in R software using "survival" package [39] and reported results as hazard ratio (HR) per 1–standard deviation increase in risk score and 95% confidence interval. The association of single variants with AD and MCI was assessed using a logistic regression model adjusted for age and sex. Results of association analyses were reported as unstandardized regression coefficient and *P* values.

To test the association of MRI phenotypes including total brain volume, white matter lesions, and hippocampal volume with the risk scores, we used linear regression adjusted for age, sex, and intracranial volume in MRI scans. Single-variant association analysis was also performed for MRI phenotypes. Bonferroni correction [0.05/(11 risk scores × 5 phenotypes); $P = 9.09 \times 10^{-4}$] was used to correct for multiple testing.

3. Results

3.1. Association of the GRS1 with AD, MCI, and MRI endophenotypes

The risk score containing all SNPs, that is, GRS1 both including *APOE* ε4 (effect = 0.73, $P = 6.53 \times 10^{-74}$)

Table 3
Results of association of MCI with risk scores

SNP cluster*	Including *APOE*			Excluding *APOE*		
	β	SE	*P* value	β	SE	*P* value
GRS1 (combined)	0.19	0.075	.012	0.59	0.179	9.51×10^{-4}
Immune response	-	-	-	0.46	0.295	.116
Endocytosis	-	-	-	1.16	0.305	1.44×10^{-4}
Cholesterol transport	0.11	0.082	.164	0.39	0.392	.322
Hematopoietic cell lineage†	0.09	0.084	.269	-	-	-
Hemostasis	-	-	-	−0.08	0.524	.872
Clathrin/AP2 adaptor complex	0.12	0.082	.128	0.72	0.423	.089
Protein folding†	0.10	0.083	.218	-	-	-

Abbreviations: β, regression coefficient; APOE, apolipoprotein E; GRS1, combined genetic risk score; GRS2, pathway-specific genetic risk score; SE, standard error; SNP, single-nucleotide polymorphism; RS, Rotterdam Study.

NOTE. Multiple testing correction by Bonferroni [0.05/(5 phenotypes × 11 risk scores); $P < 9.09 \times 10^{-4}$] was considered significant.

*Logistic regression model adjusted for age and sex in the RS (N = 360 cases).

†Only one SNP available in excluding *APOE* pathway-based GRS2.

Table 4
Results for association of risk scores with MRI phenotypes

	Including *APOE*									Excluding *APOE*								
	White matter lesions			Hippocampal volume			Brain volume			White matter lesions			Hippocampal volume			Brain volume		
SNP cluster*	β	SE	*P*	β	SE	*P*	β	SE	*P*	β	SE	*P*	β	SE	*P*	β	SE	*P*
GRS1 (combined)	0.012	0.016	.448	−0.001	0.016	.929	0.002	0.007	.806	0.059	0.037	.114	−0.009	0.038	.810	−0.006	0.016	.724
Immune response	-	-	-	-	-	-	-	-	-	0.149	0.062	.016	−0.024	0.062	.706	−0.010	0.026	.692
Endocytosis	-	-	-	-	-	-	-	-	-	0.071	0.062	.254	−0.046	0.063	.462	0.004	0.026	.865
Cholesterol transport	0.005	0.017	.785	0.001	0.017	.964	0.004	0.007	.574	0.063	0.080	.434	0.013	0.080	.875	0.023	0.033	.497
Hematopoietic cell lineage†	0.002	0.017	.901	0.001	0.017	.976	0.004	0.007	.556	-	-	-	-	-	-	-	-	-
Hemostasis	-	-	-	-	-	-	-	-	-	0.228	0.108	.034	−0.077	0.109	.479	−0.009	0.045	.835
Clathrin/AP2 adaptor complex	0.011	0.017	.507	−0.002	0.017	.924	0.003	0.007	.658	0.258	0.088	3.55×10^{-3}	−0.077	0.109	.479	−0.009	0.045	.835
Protein folding†	0.007	0.017	.700	−0.001	0.017	.970	0.004	0.007	.619	-	-	-	-	-	-	-	-	-

Abbreviations: β, regression coefficient; APOE, apolipoprotein E; GRS1, combined genetic risk score; GRS2, pathway-specific genetic risk score; MRI, magnetic resonance imaging; SE, standard error; SNP, single-nucleotide polymorphism; RS, Rotterdam Study.

NOTE. Multiple testing correction by Bonferroni [0.05/(5 phenotypes × 11 risk scores); $P < 9.09 \times 10^{-4}$] was considered significant.

*Linear regression model with MRI phenotype as outcome and risk score as predictor, adjusted for age at MRI scan and sex in the RS (N = 4521).

†Only one SNP available in excluding *APOE* pathway-based GRS2.

and excluding *APOE* ε4 (effect = 0.69, $P = 1.12 \times 10^{-11}$), was significantly associated with an increased risk of AD (Table 2). This association remained significant (*APOE* excluding; effect = 0.66, $P = 8.45 \times 10^{-7}$) after removing the patients who were included in the IGAP meta-analysis [7] (Supplementary Table 3). GRS1 was also significantly associated with progression from normal subjects into AD patients both including (HR = 1.69, $P = 6.64 \times 10^{-83}$) and excluding *APOE* ε4 (HR = 1.27, $P = 4.88 \times 10^{-15}$; Supplementary Table 4). GRS1 was associated with MCI when *APOE* ε4 was included (effect = 0.19, $P = .012$), but the association was stronger when *APOE* ε4 was excluded from the analysis (effect = 0.59, $P = 9.51 \times 10^{-4}$; Table 3); however, these associations did not pass multiple testing correction. No association of GRS1 was observed with any of the MRI phenotypes: white matter lesions, hippocampal volume, and total brain volume (Table 4).

3.2. Association of the GRS2 with AD

Among GRS2 of which *APOE* ε4 is a part, *cholesterol transport*, *hematopoietic cell lineage*, *clathrin/AP2 adaptor complex,* and *protein folding* were significantly associated with AD (effect ≥ 0.71, $P < 3.22 \times 10^{-64}$) only when *APOE* ε4 was included in the risk scores. Among the non-*APOE* pathways, AD was significantly associated with GRS2 capturing *immune response* (effect = 0.69, $P = 3.20*10^{-5}$) and *endocytosis pathway* (effect = 0.75, $P = 1.28 \times 10^{-5}$; Table 2), and association sustained (*immune response*: effect = 0.68, $P = 2.22 \times 10^{-3}$, and *endocytosis*: effect = 0.79, $P = 5.37 \times 10^{-4}$) even after removing the patients who were included in the IGAP meta-analysis [7] (Supplementary Table 3). GRS2 capturing *immune response* (HR = 1.14, $P = 1.19 \times 10^{-5}$), *endocytosis* (HR = 1.19, $P = 5.16 \times 10^{-8}$), and *APOE* ε4-excluded *clathrin/AP2 adaptor complex* (HR = 1.09, $P = 5.98 \times 10^{-3}$) pathway showed association with progression from normal into AD. Both *Immune response* and *endocytosis* pathways were significant after correcting for multiple testing. GRS2 including *APOE* ε4 were also significantly associated with normal-to-AD progression (HR ≥ 1.60, $P \leq 1.44 \times 10^{-69}$; Supplementary Table 4). Comparatively, except for *APOE* ε4, and the variants in *CR1* and *BIN1* genes, no single variant showed significant evidence of association with AD (Supplementary Table 5). The variant rs6733839 in the *BIN1* gene partially explains the association between the *endocytosis* pathway and AD, whereas *APOE* ε4 mainly explains the association of all pathways of which *APOE* ε4 is a part.

3.3. Association of the GRS2 with MCI

In GRS2, only the *endocytosis* pathway showed significant evidence for association (effect = 1.16, $P = 1.44 \times 10^{-4}$; Table 3) with MCI. Although the significance of the association is similar to that of the overall risk score (GRS1), the effect estimate is considerably higher (1.16 vs. 0.59 overall). In the single-variant analysis, the strongest association of MCI was observed with rs6733839 in the *BIN1* gene (effect = 0.262, $P = 1.12 \times 10^{-3}$; Supplementary Table 5). Although this association was not significant after correcting for multiple testing, however, it partially explains the association between MCI and GRS2 capturing *endocytosis*.

3.4. Association of the GRS2 with MRI phenotypes

White matter lesions were associated with GRS2 capturing *immune response* (effect = 0.15, $P = .016$) and

clathrin/AP2 adaptor complex excluding *APOE* ε4 (effect = 0.26, $P = 3.55 \times 10^{-3}$). If we consider multiple testing, both these associations lose significance after accounting for all tested phenotypes and risk scores. Of note is that no association of white matter lesions with the GRS2 capturing the *clathrin/AP2 adaptor complex* is observed when *APOE* ε4 is included in the GRS2 (effect = 0.011, $P = .507$; Table 4). We did not observe association of GRS2 with hippocampal volume and total brain volume. In the single-variant analysis, association of white matter lesions is seen with variants in *PICALM* and *CLU* genes ($P \leq .05$). Hippocampal volume shows association with variants in *BIN1* and *CELF1* genes ($P < .05$; Supplementary Table 6). None of the single-variant association sustained Bonferroni correction for multiple testing.

4. Discussion

Combined risk score is significantly associated with AD and normal-to-AD progression but not with any of the early features of AD tested in our study including MCI and MRI markers. However, our pathway-based risk score analysis shows that the *endocytosis* pathway significantly associates with MCI in addition to AD and normal-to-AD progression (Supplementary Fig. 1).

The association of GRS1 with AD is consistent with other similar studies on AD [40–42]. However, while others observed significant association of combined risk score with MCI [43,44], in our study the association of GRS1 with MCI was not significant after correcting for multiple testing. We did not find association of GRS1 with any of the studied MRI endophenotypes. These findings are consistent with those of Mormino et al. [45] and Lupton et al. [46]; both studies did not find association of hippocampal volume with combined GRS1 based on genome-wide significant AD variants, but Mormino et al. [45], observed this association only with risk score based on non–genome wide significant AD variants. The largest study so far that included the RS, however, reported significant evidence of association of risk score based on all genome-wide significant AD variants with hippocampal volume and total brain volume [47].

This is the first study that addressed the role of specific pathways in AD and its early clinical manifestations, that is, MCI and MRI phenotypes. Our study shows that GRS2 based on the *immune response* pathway was significantly associated with AD and normal-to-AD progression. Furthermore, we observed association of *immune response* with white matter lesions at MRI, but this association did not survive Bonferroni correction. The genes clustered in the *immune response* pathway (*CLU, CRI, INPP5D, MS4A6A, TREM2, MEF2C, and EPHA1*) are mainly expressed in microglial cells and play a part in the innate *immune response* in the central nervous system [48–52]. Microglial cells are also thought to play a role in amyloid plaque clearance [53,54]. It has been hypothesized that the activation of the immune system and the subsequent inflammatory response are involved in neuronal damage including axonal loss and white matter pathology due to demyelination [55]. White matter lesions are associated with increased risk of cognitive decline, developing dementia [21] and AD [22,56]. White matter lesions are also more frequently observed in AD patients than controls [57,58].

The most interesting finding of the present study is that the genes capturing the *endocytosis* pathway significantly associate to MCI, AD, and with progression from normal (dementia free) to AD. This pathway is independent of *APOE* and includes the *BIN1, PICALM, CD2AP, and SORL1* genes. We show that the association of GRS1 with MCI status is mainly attributed to the genes involved in the *endocytosis* pathway. Omitting the AD genes not related to the *endocytosis* pathway makes the association of the pathway with MCI even stronger. This suggests that the *endocytosis* pathway plays a critical role in an early prodromal phase of AD. Our findings are in line with previous studies suggesting the activation of the *endocytic* pathway is the earliest reported intracellular manifestation of AD [59–61]. Furthermore, the effect estimate of the *endocytosis* pathway was larger for MCI (1.16) compared with AD (0.75), suggesting a stronger association with MCI; however, this difference in effect estimates was not significant ($P = .12$). The *endocytosis* pathway is involved in neuronal uptake of macromolecules and secretory vesicles during synaptic transmission. As efficient uptake of extracellular cholesterol is critical for neuronal functions such as repair, synapse formation, and exon elongation [62], normal neuronal work needs smooth functioning of *endocytosis* pathway [63]. Postmortem studies have also demonstrated reduced brain cholesterol levels in the brain areas responsible for memory and learning, among late-onset AD cases and age-matched controls [64]. These facts suggest that defects in *endocytosis,* which derive the cholesterol uptake, could lead to impaired neurotransmitter release and synaptic function [65]. Dysfunction in *endocytosis* can also contribute to accumulation of abnormal amyloid β (Aβ) peptides [66]. Based on this finding, we can suggest that the *endocytosis* pathway is a common molecular mechanism between MCI and AD that starts manifesting at early stages of disease. Risk contributed by variants clustered in this pathway at various stages of AD progression can possibly provide clue about disease trajectory.

Our study further shows association of the *clathrin/AP2 adaptor complex* pathway with white matter lesions. Although the association failed to pass the multiple testing, it is interesting to note that no association was detected with the combined risk score either in our study or a larger study performed earlier by Chauhan et al. [47] that included up to 11,550 individuals. This suggests that pathway-based risk scores may be more sensitive in picking association signals

that may be relevant for specific AD pathologies. Two variants tagging *PICALM* and *CLU* genes cluster in the c*lathrin/AP2 adaptor complex* pathway. Each variant independently shows nominal association with white matter lesions in our analyses, but combining their effect are additive and improve the strength of the association. There is a strong evidence that the two proteins encoded by the genes interact at molecular level [67,68]. *PICALM* is involved in VAMP2 trafficking that is a crucial process to maintain functional integrity of synapses, which are crucial to cognitive function [69,70]. *PICALM* is also found to be expressed in the white matter, and immunolabeling of human brain tissue shows that *PICALM* is mainly found in blood vessel walls [71]. *CLU* clustered in the *clathrin/AP2 adaptor* is involved in efflux of free insoluble Aβ peptides through blood-brain barrier [72]. Increased plasma levels of *CLU* were associated with increased burden of Aβ peptides in healthy elderly population and brain atrophy in AD [73,74] and decreased integrity of white matter in young adults [75]. Demyelination of white matter is reported to occur even before the accumulation of Aβ plaques and neurofibrillary tangles [76]. The findings of the present study suggest that the increased genetic burden of risk variants in the *clathrin/AP2 adaptor* complex (*clathrin-mediated endocytosis*) and *immune response* pathway may play a role in early pathogenesis of AD through white matter pathology.

Among pathways including *APOE* (*cholesterol transport, hematopoietic cell lineage, clathrin/AP2 adaptor complex, and protein folding*), significant association with AD and normal-to-AD progression suggests that *APOE* ε4 appears to be the driving genetic factor for these associations.

Our study provides a readout of pathway-based risk score association with AD and its predementia endophenotypes. Our findings are important from a clinical perspective as these will aid in determining whether a certain biological pathway is involved in a patient. This will permit targeted interventions based on predicted pathological pathways. Similar as the case of cardiovascular diseases [77], a heterogeneous disease treatment can be followed based on pathway biomarkers (e.g., glucose level, total cholesterol and high-density lipid levels, and liver enzymes in case of cardiovascular disease) [78] but rather on genetic basis. This requires reference pathways and treatment portfolio. In the meantime, the pathway-based genetic risk score will allow stratification of patients in clinical trials based on causal pathways involved in patients. This may improve both the power and efficiency of future clinical and preventive trials.

Our study is a step forward to use known genetic and pathway information for disentangling the mechanisms of AD, but it has one major limitation that pathway information is based on known AD variants identified so far. This will further improve in future with improved genetic risk information that can better capture the underlying pathways. Another possible limitation of our study is that 625 cases of RS-I was a part of meta-analysis performed by the IGAP [7], which can contribute to possible inflation in our results of association of risk score with AD. However, excluding these patients, the results of this study largely remained unchanged.

To conclude, our study provides strong evidence that the *endocytosis* pathway is relevant in the prodromal phase of AD, that is, in subjects with MCI. Furthermore, the pathways including *immune response* and *clathrin/AP2 adaptor complex* pathways may be relevant for brain-related early endophenotypes of AD, such as white matter lesions; this, however, needs further investigation in larger samples. Interestingly, all the observed associations with early AD pathology are shown by *APOE*-excluding pathways. Future findings from genomic research will improve the quality of the pathway-specific genetic scores.

Acknowledgments

This study was funded by the Netherlands Organisation for Health Research and Development (ZonMW) as part of the Joint Programming for Neurological Disease (JPND) as part of the PERADES Program (Defining Genetic, Polygenic, and Environmental Risk for Alzheimer's disease, using multiple powerful cohorts, focused Epigenetics and Stem cell metabolomics), Project number 733051021. This work was funded also by the European Union Innovative Medicine Initiative (IMI) programme under grant agreement No. 115975 as part of the Alzheimer's Disease Apolipoprotein Pathology for Treatment Elucidation and Development (ADAPTED, https://www.imi-adapted.eu); and the European Union's Horizon 2020 research and innovation programme as part of the Common mechanisms and pathways in Stroke and Alzheimer's disease CoSTREAM project (www.costream.eu, grant agreement No. 667375); European Union's Horizon 2020 research and innovation programme Marie Skłodowska-Curie Research and Innovation Staff Exchange (RISE) under the grant agreement No. 645740 as part of the Personalized pREvention of Chronic DIseases (PRECeDI) project. This study was also supported by MRC Dementias Platform UK (DPUK) and the UK Dementia Research Institute (UK DRI). The Rotterdam Study is funded by the Erasmus Medical Center and Erasmus University, Rotterdam; Netherlands Organization for the Health Research and Development (ZonMw); the Research Institute for Diseases in the Elderly (RIDE), the Ministry of Education, Culture, and Science; the Ministry for Health, Welfare and Sports; the European Commission (DG XII); and the Municipality of Rotterdam. The authors are grateful to the study participants, the staff from the Rotterdam Study, and the participating general practitioners and pharmacists. The generation and management of GWAS genotype data for the Rotterdam Study (RS-I, RS-II, RS-III) was executed by the Human Genotyping Facility of the Genetic

Laboratory of the Department of Internal Medicine, Erasmus MC, Rotterdam, The Netherlands. The GWAS data sets are supported by the Netherlands Organization of Scientific Research NWO Investments (Project number 175.010.2005.011, 911-03-012), the Genetic Laboratory of the Department of Internal Medicine, Erasmus MC, the Research Institute for Diseases in the Elderly (014-93-015; RIDE2), and the Netherlands Genomics Initiative (NGI)/ Netherlands Organization for Scientific Research (NWO) Netherlands Consortium for Healthy Aging (NCHA), project number 050-060-810. We thank Pascal Arp, Mila Jhamai, Marijn Verkerk, Lizbeth Herrera, and Marjolein Peters, MSc, and Carolina Medina-Gomez, MSc, for their help in creating the GWAS database, and Karol Estrada, PhD, Yurii Aulchenko, PhD, and Carolina Medina-Gomez, MSc, for the creation and analysis of imputed data. I would like to thanks Alzheimer Nederland for providing me travel grant to present my research at AAIC2017.

Supplementary data

Supplementary data related to this article can be found at https://doi.org/10.1016/j.jalz.2018.01.005.

RESEARCH IN CONTEXT

1. Systematic review: For constructing genetic risk scores, we classified genome-wide significant Alzheimer's disease risk variants into seven diverse biological pathways based on literature identified using Google Scholar and PubMed resources.
2. Interpretation: In a large prospective population-based cohort, we evaluated the role of pathway-based genetic risk scores in predementia endophenotypes including mild cognitive impairment and brain magnetic resonance imaging phenotypes. Genetic risk scores capturing the *endocytosis* pathway was significantly associated with mild cognitive impairment, and the *clathrin/AP2 adaptor complex* pathway also showed evidence of modest association with white matter lesions. This study provides a differential role of biological pathways during the clinically heterogeneous predementia phase of Alzheimer's disease.
3. Future directions: In addition to replication of these findings in a larger independent population, this research can be extended to include all non–genome wide significant variants in these pathways. Furthermore, the results of this study could help to prioritize targets for early intervention in the disease process.

References

[1] Gatz M, Reynolds CA, Fratiglioni L, Johansson B, Mortimer JA, Berg S, et al. Role of genes and environments for explaining Alzheimer disease. Arch Gen Psychiatry 2006;63:168–74.
[2] Corder EH, Saunders AM, Strittmatter WJ, Schmechel DE, Gaskell PC, Small GW, et al. Gene dose of apolipoprotein E type 4 allele and the risk of Alzheimer's disease in late onset families. Science 1993;261:921–3.
[3] Bu G. Apolipoprotein E and its receptors in Alzheimer's disease: pathways, pathogenesis and therapy. Nat Rev Neurosci 2009;10:333–44.
[4] Huang Y, Mucke L. Alzheimer mechanisms and therapeutic strategies. Cell 2012;148:1204–22.
[5] Kopke E, Tung YC, Shaikh S, Alonso AC, Iqbal K, Grundke-Iqbal I. Microtubule-associated protein tau. Abnormal phosphorylation of a non-paired helical filament pool in Alzheimer disease. J Biol Chem 1993;268:24374–84.
[6] Hardy JA, Higgins GA. Alzheimer's disease: the amyloid cascade hypothesis. Science 1992;256:184–5.
[7] Lambert JC, Ibrahim-Verbaas CA, Harold D, Naj AC, Sims R, Bellenguez C, et al. Meta-analysis of 74,046 individuals identifies 11 new susceptibility loci for Alzheimer's disease. Nat Genet 2013;45:1452–8.
[8] Genin E, Hannequin D, Wallon D, Sleegers K, Hiltunen M, Combarros O, et al. APOE and Alzheimer disease: a major gene with semi-dominant inheritance. Mol Psychiatry 2011;16:903–7.
[9] Lambert JC, Heath S, Even G, Campion D, Sleegers K, Hiltunen M, et al. Genome-wide association study identifies variants at CLU and CR1 associated with Alzheimer's disease. Nat Genet 2009;41:1094–9.
[10] Seshadri S, Fitzpatrick AL, Ikram MA, DeStefano AL, Gudnason V, Boada M, et al. Genome-wide analysis of genetic loci associated with Alzheimer disease. JAMA 2010;303:1832–40.
[11] Hollingworth P, Harold D, Sims R, Gerrish A, Lambert JC, Carrasquillo MM, et al. Common variants at ABCA7, MS4A6A/MS4A4E, EPHA1, CD33 and CD2AP are associated with Alzheimer's disease. Nat Genet 2011;43:429–35.
[12] Naj AC, Jun G, Beecham GW, Wang LS, Vardarajan BN, Buros J, et al. Common variants at MS4A4/MS4A6E, CD2AP, CD33 and EPHA1 are associated with late-onset Alzheimer's disease. Nat Genet 2011;43:436–41.
[13] Desikan RS, Schork AJ, Wang Y, Thompson WK, Dehghan A, Ridker PM, et al. Polygenic overlap between C-reactive protein, plasma lipids, and Alzheimer disease. Circulation 2015;131:2061–9.
[14] Guerreiro R, Bras J, Hardy J. SnapShot: genetics of Alzheimer's disease. Cell 2013;155:968–968.e1.
[15] Medway C, Morgan K. Review: The genetics of Alzheimer's disease; putting flesh on the bones. Neuropathol Appl Neurobiol 2014;40:97–105.
[16] International Genomics of Alzheimer's Disease Consortium. Convergent genetic and expression data implicate immunity in Alzheimer's disease. Alzheimers Dement 2015;11:658–71.
[17] Van der Flier WM. Clinical heterogeneity in familial Alzheimer's disease. Lancet Neurol 2016;15:1296–8.
[18] Becker JT, Huff FJ, Nebes RD, Holland A, Boller F. Neuropsychological function in Alzheimer's disease. Pattern of impairment and rates of progression. Arch Neurol 1988;45:263–8.
[19] Mann UM, Mohr E, Gearing M, Chase TN. Heterogeneity in Alzheimer's disease: progression rate segregated by distinct neuropsychological and cerebral metabolic profiles. J Neurol Neurosurg Psychiatry 1992;55:956–9.
[20] Dubois B, Hampel H, Feldman HH, Scheltens P, Aisen P, Andrieu S, et al. Preclinical Alzheimer's disease: definition, natural history, and diagnostic criteria. Alzheimers Dement 2016;12:292–323.
[21] Debette S, Beiser A, DeCarli C, Au R, Himali JJ, Kelly-Hayes M, et al. Association of MRI markers of vascular brain injury with incident stroke, mild cognitive impairment, dementia, and mortality: the Framingham Offspring Study. Stroke 2010;41:600–6.

[22] Debette S, Markus HS. The clinical importance of white matter hyperintensities on brain magnetic resonance imaging: systematic review and meta-analysis. BMJ 2010;341:c3666.
[23] Kaye JA, Swihart T, Howieson D, Dame A, Moore MM, Karnos T, et al. Volume loss of the hippocampus and temporal lobe in healthy elderly persons destined to develop dementia. Neurology 1997; 48:1297–304.
[24] Petersen RC, Smith GE, Waring SC, Ivnik RJ, Tangalos EG, Kokmen E. Mild cognitive impairment: clinical characterization and outcome. Arch Neurol 1999;56:303–8.
[25] Gauthier S, Reisberg B, Zaudig M, Petersen RC, Ritchie K, Broich K, et al. Mild cognitive impairment. Lancet 2006;367:1262–70.
[26] Petersen RC. Mild cognitive impairment as a diagnostic entity. J Intern Med 2004;256:183–94.
[27] Hofman A, Brusselle GG, Darwish Murad S, van Duijn CM, Franco OH, Goedegebure A, et al. The Rotterdam Study: 2016 objectives and design update. Eur J Epidemiol 2015;30:661–708.
[28] McCarthy S, Das S, Kretzschmar W, Delaneau O, Wood AR, Teumer A, et al. A reference panel of 64,976 haplotypes for genotype imputation. Nat Genet 2016;48:1279–83.
[29] Das S, Forer L, Schonherr S, Sidore C, Locke AE, Kwong A, et al. Next-generation genotype imputation service and methods. Nat Genet 2016;48:1284–7.
[30] Delaneau O, Marchini J, Genomes Project C, Genomes Project C. Integrating sequence and array data to create an improved 1000 Genomes Project haplotype reference panel. Nat Commun 2014;5:3934.
[31] Howie B, Fuchsberger C, Stephens M, Marchini J, Abecasis GR. Fast and accurate genotype imputation in genome-wide association studies through pre-phasing. Nat Genet 2012;44:955–9.
[32] Ikram MA, van der Lugt A, Niessen WJ, Koudstaal PJ, Krestin GP, Hofman A, et al. The Rotterdam Scan Study: design update 2016 and main findings. Eur J Epidemiol 2015;30:1299–315.
[33] Vrooman HA, Cocosco CA, van der Lijn F, Stokking R, Ikram MA, Vernooij MW, et al. Multi-spectral brain tissue segmentation using automatically trained k-Nearest-Neighbor classification. Neuroimage 2007;37:71–81.
[34] De Boer R, Vrooman HA, Van Der Lijn F, Vernooij MW, Ikram MA, Van Der Lugt A, et al. White matter lesion extension to automatic brain tissue segmentation on MRI. Neuroimage 2009;45:1151–61.
[35] Fischl B. FreeSurfer. Neuroimage 2012;62:774–81.
[36] Klein S, Staring M, Pluim JPW. Comparison of gradient approximation techniques for optimisation of mutual information in nonrigid registration. 2005. p. 192–203.
[37] Ikram MA, Fornage M, Smith AV, Seshadri S, Schmidt R, Debette S, et al. Common variants at 6q22 and 17q21 are associated with intracranial volume. Nat Genet 2012;44:539–44.
[38] Guerreiro R, Wojtas A, Bras J, Carrasquillo M, Rogaeva E, Majounie E, et al. TREM2 variants in Alzheimer's disease. N Engl J Med 2013;368:117–27.
[39] Therneau T. A Package for Survival Analysis in S. R package version 2.37-7. 2014. Available at: http://CRAN R-project.org/package=survival; 2015. Accessed May 28, 2017.
[40] Chouraki V, Reitz C, Maury F, Bis JC, Bellenguez C, Yu L, et al. Evaluation of a genetic risk score to improve risk prediction for Alzheimer's disease. J Alzheimers Dis 2016;53:921–32.
[41] Escott-Price V, Shoai M, Pither R, Williams J, Hardy J. Polygenic score prediction captures nearly all common genetic risk for Alzheimer's disease. Neurobiol Aging 2016;49:214.e7–214.e11.
[42] Sleegers K, Bettens K, De Roeck A, Van Cauwenberghe C, Cuyvers E, Verheijen J, et al. A 22-single nucleotide polymorphism Alzheimer's disease risk score correlates with family history, onset age, and cerebrospinal fluid Aβ42. Alzheimers Dement 2015;11:1452–60.
[43] Adams HH, de Bruijn RF, Hofman A, Uitterlinden AG, van Duijn CM, Vernooij MW, et al. Genetic risk of neurodegenerative diseases is associated with mild cognitive impairment and conversion to dementia. Alzheimers Dement 2015;11:1277–85.
[44] Lacour A, Espinosa A, Louwersheimer E, Heilmann S, Hernandez I, Wolfsgruber S, et al. Genome-wide significant risk factors for Alzheimer's disease: role in progression to dementia due to Alzheimer's disease among subjects with mild cognitive impairment. Mol Psychiatry 2017;22:153–60.
[45] Mormino EC, Sperling RA, Holmes AJ, Buckner RL, De Jager PL, Smoller JW, et al. Polygenic risk of Alzheimer disease is associated with early- and late-life processes. Neurology 2016;87:481–8.
[46] Lupton MK, Strike L, Hansell NK, Wen W, Mather KA, Armstrong NJ, et al. The effect of increased genetic risk for Alzheimer's disease on hippocampal and amygdala volume. Neurobiol Aging 2016;40:68–77.
[47] Chauhan G, Adams HH, Bis JC, Weinstein G, Yu L, Toglhofer AM, et al. Association of Alzheimer's disease GWAS loci with MRI markers of brain aging. Neurobiol Aging 2015; 36:1765.e7–1765.e16.
[48] Zhang Y, Chen K, Sloan SA, Bennett ML, Scholze AR, O'Keeffe S, et al. An RNA-sequencing transcriptome and splicing database of glia, neurons, and vascular cells of the cerebral cortex. J Neurosci 2014;34:11929–47.
[49] Kofler J, Bissel S, Wiley C, Stauffer M, Murdoch G. Differential microglial expression of new Alzheimer's disease associated genes MS4A4A and MS4A6A. Alzheimers Dement 2012;8:P253.
[50] Colonna M. TREMs in the immune system and beyond. Nat Rev Immunol 2003;3:445–53.
[51] Crehan H, Hardy J, Pocock J. Blockage of CR1 prevents activation of rodent microglia. Neurobiol Dis 2013;54:139–49.
[52] Zhang B, Gaiteri C, Bodea LG, Wang Z, McElwee J, Podtelezhnikov AA, et al. Integrated systems approach identifies genetic nodes and networks in late-onset Alzheimer's disease. Cell 2013;153:707–20.
[53] Lee CY, Landreth GE. The role of microglia in amyloid clearance from the AD brain. J Neural Transm (Vienna) 2010;117:949–60.
[54] Heneka MT, Carson MJ, El Khoury J, Landreth GE, Brosseron F, Feinstein DL, et al. Neuroinflammation in Alzheimer's disease. Lancet Neurol 2015;14:388–405.
[55] Heppner FL, Ransohoff RM, Becher B. Immune attack: the role of inflammation in Alzheimer disease. Nat Rev Neurosci 2015; 16:358–72.
[56] Jeong H, Son S, Kim SK, Park KJ, Choi NC, Kwon OY, et al. Age, hypertension, and genetic polymorphisms and their relative associations with white matter hyperintensities in Korean patients with Alzheimer's disease. Neurol Asia 2015;20:35–41.
[57] Smith EE, Egorova S, Blacker D, Killiany RJ, Muzikansky A, Dickerson BC, et al. Magnetic resonance imaging white matter hyperintensities and brain volume in the prediction of mild cognitive impairment and dementia. Arch Neurol 2008;65:94–100.
[58] Wolf H, Ecke GM, Bettin S, Dietrich J, Gertz HJ. Do white matter changes contribute to the subsequent development of dementia in patients with mild cognitive impairment? A longitudinal study. Int J Geriatr Psychiatry 2000;15:803–12.
[59] Funderburk SF, Marcellino BK, Yue Z. Cell "self-eating" (autophagy) mechanism in Alzheimer's disease. Mt Sinai J Med 2010;77:59–68.
[60] Ginsberg SD, Mufson EJ, Alldred MJ, Counts SE, Wuu J, Nixon RA, et al. Upregulation of select rab GTPases in cholinergic basal forebrain neurons in mild cognitive impairment and Alzheimer's disease. J Chem Neuroanat 2011;42:102–10.
[61] Cataldo AM, Peterhoff CM, Troncoso JC, Gomez-Isla T, Hyman BT, Nixon RA. Endocytic pathway abnormalities precede amyloid beta deposition in sporadic Alzheimer's disease and Down syndrome: differential effects of APOE genotype and presenilin mutations. Am J Pathol 2000;157:277–86.
[62] Vance JE, Campenot RB, Vance DE. The synthesis and transport of lipids for axonal growth and nerve regeneration. Biochim Biophys Acta 2000;1486:84–96.

[63] Keating DJ, Chen C, Pritchard MA. Alzheimer's disease and endocytic dysfunction: clues from the Down syndrome-related proteins, DSCR1 and ITSN1. Ageing Res Rev 2006;5:388–401.
[64] Svennerholm L, Gottfries CG. Membrane lipids, selectively diminished in Alzheimer brains, suggest synapse loss as a primary event in early-onset form (type I) and demyelination in late-onset form (type II). J Neurochem 1994;62:1039–47.
[65] Woodruff G, Reyna SM, Dunlap M, Van Der Kant R, Callender JA, Young JE, et al. Defective transcytosis of APP and lipoproteins in human iPSC-derived neurons with familial Alzheimer's disease mutations. Cell Rep 2016;17:759–73.
[66] Maxfield FR. Role of endosomes and lysosomes in human disease. Cold Spring Harb Perspect Biol 2014;6:a016931.
[67] Yang X, Li J, Liu B, Li Y, Jiang T. Impact of PICALM and CLU on hippocampal degeneration. Hum Brain Mapp 2016;37:2419–30.
[68] Tan L, Wang HF, Tan MS, Tan CC, Zhu XC, Miao D, et al. Effect of CLU genetic variants on cerebrospinal fluid and neuroimaging markers in healthy, mild cognitive impairment and Alzheimer's disease cohorts. Sci Rep 2016;6:26027.
[69] Harel A, Wu F, Mattson MP, Morris CM, Yao PJ. Evidence for CALM in directing VAMP2 trafficking. Traffic 2008;9:417–29.
[70] Yao PJ. Synaptic frailty and clathrin-mediated synaptic vesicle trafficking in Alzheimer's disease. Trends Neurosci 2004;27:24–9.
[71] Baig S, Joseph SA, Tayler H, Abraham R, Owen MJ, Williams J, et al. Distribution and expression of PICALM in Alzheimer disease. J Neuropathol Exp Neurol 2010;69:1071–7.
[72] Zlokovic BV. Neurovascular pathways to neurodegeneration in Alzheimer's disease and other disorders. Nat Rev Neurosci 2011;12:723–38.
[73] Thambisetty M, Simmons A, Velayudhan L, Hye A, Campbell J, Zhang Y, et al. Association of plasma clusterin concentration with severity, pathology, and progression in Alzheimer disease. Arch Gen Psychiatry 2010;67:739–48.
[74] Weinstein G, Beiser AS, Preis SR, Courchesne P, Chouraki V, Levy D, et al. Plasma clusterin levels and risk of dementia, Alzheimer's disease, and stroke. Alzheimers Dement (Amst) 2016;3:103–9.
[75] Braskie MN, Jahanshad N, Stein JL, Barysheva M, McMahon KL, de Zubicaray GI, et al. Common Alzheimer's disease risk variant within the CLU gene affects white matter microstructure in young adults. J Neurosci 2011;31:6764–70.
[76] Sachdev PS, Zhuang L, Braidy N, Wen W. Is Alzheimer's a disease of the white matter? Curr Opin Psychiatry 2013;26:244–51.
[77] Sun X, Jia Z. A brief review of biomarkers for preventing and treating cardiovascular diseases. J Cardiovasc Dis Res 2012;3:251–4.
[78] Upadhyay RK. Emerging risk biomarkers in cardiovascular diseases and disorders. J Lipids 2015;2015:971453.